Amendments to the Claims

This listing of claims presented hereinbelow will replace all prior versions and listings of claims in the application. Please cancel claims 101 and 113 without prejudice.

In The Claims

1-48. (Canceled)

49. (Currently amended) An isolated polynucleotide consisting of at least 8 consecutive bases [and up] to about 100 consecutive bases of [the sequence shown in] SEQ ID NOS:1 or 2, or the complement thereof, wherein said isolated polynucleotide includes at least one single nucleotide polymorphism (SNP) selected from a group consisting of [polymorphisms] SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO: 1, wherein said SNPs are found in a general human population with about 25% or less frequency.

50-52. (Canceled)

53. (Currently amended) A kit comprising [an] at least one isolated polynucleotide of Claim 49 and instructions to use the kit.

54. (Currently amended) A kit comprising at least [one pair of] two isolated polynucleotides as in [Claim 52] Claim 49.

55. (Currently amended) An isolated polynucleotide consisting of at least 18 consecutive bases [and up] to about 100 consecutive bases of [the sequence shown in] SEQ ID NOS:1 or 2, or the complement thereof, wherein said isolated polynucleotide includes at least one SNP [polymorphism] selected from a group consisting of SNPs [polymorphisms] at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO:1, wherein said SNPs are found in a general human population with about 25% or less frequency.

56-58. (Canceled)

59. (Currently amended) A kit comprising [an] at least one isolated polynucleotide of Claim 55 and instructions to use the kit.

60. (Currently amended) A kit comprising at least [one pair of] two isolated polynucleotides as in [Claim 58] Claim 55.

61. (Currently amended) An isolated polynucleotide consisting of [a fragment of] at least [about] 100 consecutive bases [and up] to about 235 consecutive kilobases of [the sequence shown in] SEQ ID NOS:1 or 2, or the complement thereof, wherein said isolated polynucleotide includes at least one SNP [polymorphism] selected from a group consisting of SNPs [polymorphisms] at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO:1, wherein said SNPs are found in a general human population with about 25% or less frequency.

62. (Previously presented) The isolated polynucleotide of Claim 61 which is cDNA.

63. (Previously presented) The isolated polynucleotide of Claim 61 which is RNA.

64. (Previously presented) The isolated polynucleotide of Claim 61 which is genomic DNA.

65. (Currently amended) An isolated polynucleotide consisting of [a fragment of] at least [about] 300 consecutive bases [and up] to about 235 consecutive kilobases of [the sequence shown in] SEQ ID NOS:1 or 2, or the complement thereof, wherein said isolated polynucleotide includes at least one SNP [polymorphism] selected from a group consisting of SNPs [polymorphisms] at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO:1, wherein said SNPs are found in a general human population with about 25% or less frequency.

66. (Previously presented) The isolated polynucleotide of Claim 65 which is cDNA.

67. (Previously presented) The isolated polynucleotide of Claim 65 which is RNA.

68. (Previously presented) The isolated polynucleotide of Claim 65 which is genomic DNA.

69-99. (Canceled)

100. (Currently amended) A kit for determining the likelihood of an individual being affected with hereditary hemochromatosis comprising,

(a) one or more oligonucleotides [each individually] comprising a sequence that hybridizes under stringent hybridization conditions to a SNP in a target nucleic acid [comprising one or more polymorphisms] at a SNP site selected from a group consisting of SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 [or] and 35983 of [SEQ. ID. NO: 1] SEQ ID NO:1; and

(b) instructions to use the kit [to determine the likelihood of said individual being affected with hereditary hemochromatosis].

101. (Canceled herein).

102. (Currently amended) The kit of [claim] Claim 100 [or 101,] wherein [one or more of the oligonucleotides] the oligonucleotide [each individually comprise a sequence that is fully complementary to a nucleic acid comprising one or more polymorphisms at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 or 35983 of SEQ. ID. NO: 1] is fully complementary to the target nucleic acid.

103. (Currently amended) The kit of [claim] Claim 100 [or 101,] further comprising sequencing primers.

104. (Currently amended) The kit of [claim] Claim 100 [or 101,] further comprising amplification primers.

105. (Currently amended) The kit of [claim] Claim 100 [or 101,] further comprising reagents for labeling one or more of the oligonucleotides.

106. (Currently amended) The kit of [claim] Claim 100 [or 101], wherein one or more of the oligonucleotides are labeled.

107. (Currently amended) The kit of [claim] Claim 106 that includes one or more reagents to detect the label.

108-109. (Cancelled)

110. (Currently amended) The kit of [claim] Claim 100 [or 101], wherein said kit is configured to detect the presence of two or more [polymorphisms] SNPs, wherein at least one of the [polymorphisms] SNPs is selected from a group consisting of [polymorphisms] SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO:1.

111. (Currently amended) The kit of [claim] Claim 100 [or 101], wherein said kit is configured to detect the presence of two or more [polymorphisms] SNPs selected from a group consisting of SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 [or] and 35983 of [SEQ. ID. NO: 1] SEQ ID NO: 1.

112. (Reintroduced) An array [for determining the likelihood of an individual being affected with hereditary hemochromatosis] comprising[,one or more] a plurality of oligonucleotides according to claim 123 immobilized on a substrate.

113. (Canceled herein).

114. (Reintroduced) The array of claim 112 [or 113], wherein [each oligonucleotide individually] the oligonucleotides are [comprises a sequence that is] fully complementary to [a] the target nucleic acid [comprising one or more polymorphisms at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 or 35983 of SEQ. ID. NO: 1.

115. (Reintroduced) The array of claim 112 [or 113], wherein one or more of the oligonucleotides are labeled.

116. (Reintroduced) The [kit] array of claim 112 [or 113], wherein [one or more of the oligonucleotides are each individually complementary to a nucleic acid comprising a polymorphism at position] the SNP is at position 35983 [of SEQ. ID.No: 1].

117. (Reintroduced) The array of claim 112 [or 113], wherein [one or more of the oligonucleotides are each individually complementary to a nucleic acid comprising a polymorphism at position] the SNP is at position 61465 [of SEQ. ID. NO: 1].

118. (Reintroduced) The array of claim 112 [or 113], wherein said array is configured to detect the presence of two or more [polymorphisms] SNPs, wherein at least one of the [polymorphisms] SNPs is selected from a group consisting of [polymorphisms] SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983 of [SEQ. ID. NO: 1] SEQ ID NO: 1.

119. (Reintroduced) The array of claim 112 [or 113], wherein said array is configured to detect the presence of two or more [polymorphisms] SNPs selected from a group of SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 [or] and 35983 of [SEQ. ID. NO: 1] SEQ ID NO: 1.

120-122. (Cancelled)

123. (New) An allele-specific oligonucleotide probe comprising a sequence of at least 8 consecutive bases that specifically hybridizes under stringent hybridization conditions to a target sequence in a nucleic acid, wherein said target sequence further comprises at least 8 consecutive bases of SEQ ID NO:1, or a complement thereof, including a SNP selected from the group of SNPs at positions 230376, 214795, 207400, 200027, 195404, 160007, 125581, 120853, 96315, 61465, 40431, 38526 and 35983.